



## RAW SEQUENCE LISTING

DATE: 03/14/2003

PATENT APPLICATION: US/08/816,011G

TIME: 12:05:33

Input Set : A:\11420122.app

Output Set: N:\CRF4\03142003\H816011G.raw

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3 <110> APPLICANT: Pausch, Mark H
4   Price, Laura A
6 <120> TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
7   AND METHODS OF USING SAME
9 <130> FILE REFERENCE: 01142.0122 SEQUENCE LISTING
11 <140> CURRENT APPLICATION NUMBER: 08/816,011G
12 <141> CURRENT FILING DATE: 1997-03-11
14 <150> PRIOR APPLICATION NUMBER: 07/332,312
15 <151> PRIOR FILING DATE: 1994-10-31
17 <150> PRIOR APPLICATION NUMBER: PCT/US95/14364
18 <151> PRIOR FILING DATE: 1995-10-25
20 <160> NUMBER OF SEQ ID NOS: 67
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2441
26 <212> TYPE: DNA
27 <213> ORGANISM: Drosophila melanogaster
29 <400> SEQUENCE: 1
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31 ctttaaaaaga aaaaaaaaaat aataagtcaa aactacaaac cacacagcga aaggcgaaag 120
32 caacgggtcc tcgcgagtgtt tattttttttt ttcaacaatt ttgatcgta gtgcgacaat 180
33 ccgtcgagca tgcgcgcgaa tcgatggatc ctgctgctca tcttctacat atcctacctg 240
34 atgttcgggg cgccaattcta ttaccatatt gagcacggcg aggagaagat atcgcgcgcc 300
35 gaacagcgca aggcgcaaat tgcaatcaac gaatatctgc tggaggagct gggcgacaag 360
36 aatacgacca cacaggatga gattcttcaa cggatctcgg attactgtga caaacgggtt 420
37 acattgccgc cgacatatga tgatacgccc tacacgtgga cttctacca tgccttcttc 480
38 ttgccttca cgttttgcgc cagcgtggga tatgggaata tatcgccaa caccttcgcc 540
39 ggacggatga tcatgatcgc gtattcgggtg attggcatcc ccgtcaatgg tatcctcttt 600
40 gccggcctcg gcgaatactt tggacgtacg tttgaagcga tctacagacg ctacaaaaag 660
41 tacaagatgt ccacggatat gcaactatgt ccgccgcagc tgggattgat caccacggtg 720
42 gtgattgccg tgattccggg aatagctctc ttcttggtgc tgccctgcgt ggggtgtcac 780
43 ctacttcgag aactgggcct atcttccatc tcgctgtact acagctatgt gaccaccaca 840
44 acaattggat tcggtgacta tgtgccaca tttggagcca accagcccaa ggagttcggc 900
45 ggctggttcg tggctctatca gatctttgtg atcgtgtggt tcatcttctc gctgggatat 960
46 cttgtgatga tcatgacatt tatcactcgg ggccctcaga gcaagaagct ggcataacctg 1020
47 gagcagcagt tgcctcccaa cctgaaggcc acacagaatc gcatctggtc tggcgtcacc 1080
48 aaggatgtgg gctacctcgg gcgaatgtct aacgagctgt acatcctcaa agtgaagcct 1140
49 gtgtacaccg atgtagatat cgcctacaca ctgccacgtt ccaattcgtg tccggatctg 1200
50 agcatgtacc gcgtggagcc ggctcccatt cccagcggga agagggcatt ctccgtgtgc 1260
51 gccgacatgg ttggcgccca aaggaggcgg ggcaggggtac acgccaattc cgatacggat 1320
52 ctaaccaaac tggatcgcca gaagacattc gagacggcgg aggcgtacca ccagaccacc 1380
53 gatttgctgg ccaaggtggt caacgcactg gccacgggtga agccaccgcc ggcggaacag 1440
54 gaagatgcgg ctctctatgg tggctatcat ggcttctccg actccagat cctggccagc 1500

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55 gaatgggtcgt tctcgacggt caacgagttc acatcaccgc gacgtccaag-ageaegtgee-1560
56 tgctccgatt tcaatctgga ggcacctcgc tggcagagcg agaggccact gcgttcgagc 1620
57 cacaacgaat ggacatggag cggcgacaac cagcagatcc aggaggcatt caaccagcgc 1680
58 tacaagggac agcagcgtgc caacggagca gccaaactcga ccatgggtcca tctggagccg 1740
59 gatgcttttg aggagcagct gagaacaat caccgggtgc cggtcgcgtc aagaagttct 1800
60 ccatgcgga tggtctgcga cgtctgtttc ccttcagaa gaagcaccoc tgcaggatc 1860
61 tggagcgcaa gttgtccgtg gtctcggtag ccgaggggtg catctcgcag gaagccagat 1920
62 ccccgctgga ctactacatc aacacggtca cggcgccctc cagtcaatcc tatttgcgca 1980
63 acggacgcgg tccgccaccg cccttcgaat cgaatggcag cttggccagc ggcggcggcg 2040
64 ggctaacgaa catgggcttc cagatggagg atggagcaac cccgccatcg gcattgggcg 2100
65 gtggagccta tcaacgcaag gcggctgctg gcaagcgccg acgcgagagc atctacacc 2160
66 agaatcaagc cccatccgct cgcgggggca gcatgtatcc gccgaccgcg cagccttg 2220
67 cccagatgca gatgcgacgc ggcagcttgg caaccagtgg ctctggatcg gcggccatg 2280
68 cggcagtggc cgcgcgtggt ggcagcctct tccagctac agcatcgga tcatcgctga 2340
69 cctctgctcc gcgcgaagc agcatattct cggttacctc cgaaaaggat atgaatgtgc 2400
70 tggagcagac gaccattgcg gatctgattc gtgcgctcga g 2441

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73 &lt;210&gt; SEQ ID NO: 2

74 &lt;211&gt; LENGTH: 618

75 &lt;212&gt; TYPE: PRT

76 &lt;213&gt; ORGANISM: Drosophila melanogaster

78 &lt;400&gt; SEQUENCE: 2

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79 Met Ser Pro Asn Arg Trp Ile Leu Leu Leu Ile Phe Tyr Ile Ser Tyr
80 1 5 10 15
82 Leu Met Phe Gly Ala Ala Ile Tyr Tyr His Ile Glu His Gly Glu Glu
83 20 25 30
85 Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
86 35 40 45
88 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
89 50 55 60
91 Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
92 65 70 75 80
94 Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
95 85 90 95
97 Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
98 100 105 110
100 Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
101 115 120 125
103 Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
104 130 135 140
106 Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
107 145 150 155 160
109 Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
110 165 170 175
112 Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
113 180 185 190
115 Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ile Ser
116 195 200 205
118 Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp Tyr
119 210 215 220

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121 Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
122 225                230                235                240
124 Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
125                245                250                255
127 Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys
128                260                265                270
130 Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
131                275                280                285
133 Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
134                290                295                300
136 Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
137 305                310                315                320
139 Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
140                325                330                335
142 Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
143                340                345                350
145 Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
146                355                360                365
148 Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
149                370                375                380
151 Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
152 385                390                395                400
154 Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
155                405                410                415
157 Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
158                420                425                430
160 Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
161                435                440                445
163 Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
164                450                455                460
166 Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
167 465                470                475                480
169 Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
170                485                490                495
172 Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
173                500                505                510
175 Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
176                515                520                525
178 Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
179                530                535                540
181 Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
182 545                550                555                560
184 Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
185                565                570                575
187 Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
188                580                585                590
190 Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg
191                595                600                605
193 Met Ala Ala Trp Pro Ala Ala Ala Ala Gly

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194 -----610-----615-----
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 1011
199 <212> TYPE: DNA
200 <213> ORGANISM: Caenorhabditis elegans
202 <400> SEQUENCE: 3
203 atgtccgatac agctgtttgt cgcatttgag aagtattttct tgaacgagtaa cgagggtcaag 60
204 aagaatgcag caacggagac atggacattt tcatcgtcca ttttctttgc cgtaaccgtc 120
205 gtcactacca tcggatacgg taatccagtt ccagtgcaca acattggacg gatatggtgt 180
206 atattgttct ccttgcttgg aatacctcta acactggtta ccacgtctga cttggcaggt 240
207 aaattcctat ctgaacatct tgtttggttg tatggaaact atttgaaatt aaaatatctc 300
208 atattgtcac gacatcgaaa agaacggaga gagcacgttt gtgagcactg tcacagtcac 360
209 ggaatggggc atgatatgaa tatcgaggag aaaagaattc ctgcattcct ggtattagct 420
210 attctgatag tatatacagc gtttggcggt gtccaatgt caaaattaga gccgtggtct 480
211 ttcttcactt cattctactg gtccttcatt acaatgacta ctgtcgggtt tggcgacttg 540
212 atgccagaaa gggacggata catgtatata atattgctct atatcatttt aggtaaattt 600
213 tcaatgaaaa aaaaacaaaa attcaaaata tttttaggtc ttgcaataac tacaatgtgc 660
214 attgatttgg taggagtaca gtatattcga aagattcatt atttcggaag aaaaattcaa 720
215 gacgctagat ctgcattggc ggttgtagga ggaaaggtag tccttgatc agaactctac 780
216 gcaaatttaa tgcaaaagcg agctcgtaac atgtcccgag aagcttttat agtggagaat 840
217 ctctatgttt ccaaacacat cataccattc ataccaactg atatccgatg tattcgatat 900
218 attgatcaaa ctgccgatgc tgctaccatt tccacgtcat cgtctgcaat tgatatgcaa 960
219 agttgtagat tttgtcattc aagatattct ctcaatcgtg cattcaaata g 1011
222 <210> SEQ ID NO: 4
223 <211> LENGTH: 336
224 <212> TYPE: PRT
225 <213> ORGANISM: Caenorhabditis elegans
227 <400> SEQUENCE: 4
228 Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
229 1 5 10 15
231 Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
232 20 25 30
234 Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
235 35 40 45
237 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
238 50 55 60
240 Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
241 65 70 75 80
243 Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
244 85 90 95
246 Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
247 100 105 110
249 Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
250 115 120 125
252 Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
253 130 135 140
255 Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
256 145 150 155 160
258 Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly

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-----259-----165-----170-----175-----
261 Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
262          180          185          190
264 Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
265          195          200          205
267 Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
268          210          215          220
270 Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
271 225          230          235          240
273 Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
274          245          250          255
276 Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
277          260          265          270
279 Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
280          275          280          285
282 Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
283          290          295          300
285 Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln
286 305          310          315          320
288 Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
289          325          330          335
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296 <211> LENGTH: 51
297 <212> TYPE: DNA
298 <213> ORGANISM: Caenorhabditis elegans
300 <400> SEQUENCE: 5
301 tccattttct ttgccgtaac cgtcgtcact accatcggat acggtaatcc a          51
304 <210> SEQ ID NO: 6
305 <211> LENGTH: 51
306 <212> TYPE: DNA
307 <213> ORGANISM: Caenorhabditis elegans
309 <400> SEQUENCE: 6
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313 <210> SEQ ID NO: 7
314 <211> LENGTH: 24
315 <212> TYPE: PRT
316 <213> ORGANISM: Drosophila melanogaster
318 <400> SEQUENCE: 7
319 Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly Tyr Gly Phe
320 1          5          10          15
322 Arg Cys Val Thr Asp Glu Cys Pro
323          20
326 <210> SEQ ID NO: 8
327 <211> LENGTH: 24
328 <212> TYPE: PRT
329 <213> ORGANISM: Drosophila melanogaster
331 <400> SEQUENCE: 8
332 Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly Tyr Gly Phe
333 1          5          10          15

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/08/816,011G

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Input Set : A:\11420122.app  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:38; Xaa Pos. 337  
Seq#:39; N Pos. 2  
Seq#:46; N Pos. 35,2057,2067,2111,2120  
Seq#:51; N Pos. 262  
Seq#:53; N Pos. 247,593,952  
Seq#:54; Xaa Pos. 88  
Seq#:56; Xaa Pos. 83,198  
Seq#:57; Xaa Pos. 1,2,3,4,5,6,8  
Seq#:58; Xaa Pos. 1,2,3,4,6,8  
Seq#:60; Xaa Pos. 6  
Seq#:61; Xaa Pos. 88  
Seq#:64; Xaa Pos. 1,2,3,4,6

## VERIFICATION SUMMARY

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Input Set : A:\11420122.app

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~~L:840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:336~~  
L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0  
L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46 after pos.:0  
M:341 Repeated in SeqNo=46  
L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:240  
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:240  
M:341 Repeated in SeqNo=53  
L:1226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:80  
L:1346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:80  
M:341 Repeated in SeqNo=56  
L:1409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0  
L:1430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0  
L:1463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60 after pos.:0  
L:1493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:80  
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64 after pos.:0